

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 18, 2001, 08:36:35 ; Search time 16.52 Seconds

(without alignments)
1198.873 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540
Sequence: 1 VYLSECKTGKNGKNGRTGMSK.....TNSQVRWEYCKRIPSCDSSPV 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Sequences: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1535	99.7	810	1	PLHU
2	1442	93.6	810	2	B30848
3	1292	83.9	790	1	PLRG
4	1281	83.8	812	1	PLBO
5	1274	82.7	812	1	PLMS
6	1237	80.3	810	2	I46260
7	881	57.2	2869	2	T18518
8	797	51.8	728	1	JH0579
9	782	50.8	728	1	A35644
10	776.5	50.4	710	1	I51283
11	776	49.4	728	1	A60185
12	766.5	49.8	716	1	JC5061
13	754.5	48.9	411	2	I51285
14	753.5	48.9	716	1	A40332
15	749	48.6	4548	1	S00657
16	739	48.0	711	1	A47136
17	739	48.0	1420	2	A32869
18	505	32.8	455	2	A61545
19	499	32.4	460	2	B61545
20	391.5	25.4	336	2	S33879
21	372	24.2	625	1	TBB0
22	362.5	23.5	169	2	A40522
23	357.5	23.2	618	2	A35827
24	351	22.8	622	1	TBBU
25	348	22.6	617	2	S10511
26	309.5	20.1	562	1	UKHRT
27	295.5	19.2	559	1	A35029
28	281.5	18.3	559	1	A29941
29	278	18.1	120	2	E61545

ALIGNMENTS

RESULT 1

PLHU
plasmin (EC 3.4.21.7) precursor [validated] - human
N:Alternate names: plasminogen precursor [misomer]
N:Contains: angiotatin; microplasmin; plasminogen
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence, revision 02-Dec-1994 #text change 15-Sep-2000
C:Accession: A35229; I52242; A26646; I62738; I64609; S03735; A00929; A04627; A04625;
R:Peterson, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
J. Biol. Chem. 265, 6104-6111, 1990
A:Title: Characterization of the gene for human plasminogen, a key proenzyme in the f
A:Reference number: A35229; M01D:90202879
A:Accession: A35229

A:Molecule type: DNA
A:Residues: 1-810 <PEP>
A:Cross-references: GB:J05286; GB:M34276; NID:9190064; PIDN:AAA60113.1; PID:9387026
A:Experimental source: leukocyte; lung fibroblast
R:Margaret, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.;
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A:Title: Definition of the transcription initiation site of human plasminogen gene in
A:Reference number: I52242; M01D:91057523
A:Accession: I52242

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <MAL1>
A:Cross-references: GB:M62890; NID:9190092; PIDN:AAA36454.1; PID:9553613
R:Forstren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FEBS Lett. 213, 254-260, 1987
A:Title: Molecular cloning and characterization of a full-length cDNA clone for human
A:Reference number: A26646; M01D:87162450
A:Accession: A26646

A:Molecule type: mRNA
A:Residues: 1-471, 'D', 473-810 <FOR>
A:Cross-references: GB:X05199; NID:935530; PIDN:CAA28631.1; PID:935531
A:Experimental source: liver
R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A:Title: Characterization of a complementary deoxyribonucleic acid coding for human a
A:Reference number: I45961; M01D:85023311
A:Accession: I62738

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 292-471, 'D', 473-810 <MAL2>
A:Cross-references: GB:K02922; NID:9190112; PIDN:AAA60124.1; PID:9387031
A:Accession: I84609

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 367-419 <MAL3>
A:Cross-references: GB:K02921; NID:9190110; PIDN:AAA60123.1; PID:9190111
R:Brundsholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lejter, W.; Manneberg,
Eur. J. Biochem. 114, 465-470, 1981
A:Title: Comparison of the primary structure of the N-terminal CNBr fragments of huma

F:79-466/Product: angiotatin #status experimental <AST>
 F:97-580/Domain: plasmin chain A #status experimental <AMT>
 F:97-580/Domain: plasmin chain A #status experimental <CHA>
 F:103-181/Domain: kringle homology <KR1>
 F:185-262/Domain: kringle homology <KR2>
 F:275-352/Domain: kringle homology <KR3>
 F:377-454/Domain: kringle homology <KR4>
 F:481-560/Domain: kringle homology <KR5>
 F:550-580,581-810/Product: microplasmin #status experimental <AMT>

Query Match 99.7%; Score 1535; DB 1: Length 810;
 Best Local Similarity 99.6%; Pred. No. 7.1e-105;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECTGNGKNGKNGYRGMTSKNGITCOKWSSTPHRRPSPATHPSEGLEENYCRPNPN 60
 |||||||
 Db 98 VYLSECTGNGKNGKNGYRGMTSKNGITCOKWSSTPHRRPSPATHPSEGLEENYCRPNPN 157
 |||||||
 QY 61 DPGSPWCYTTPDEPKRYDCILCEEECMHCSGENYDGKISKTNGLGECQAMDSQSPHAA 120
 |||||||
 Db 158 DPGSPWCYTTPDEPKRYDCILCEEECMHCSGENYDGKISKTNGLGECQAMDSQSPHAA 217
 |||||||
 QY 121 GYIPSKFPNNLKKKNYCRNPDRPWCFTTDPKRWELCDIPRCTPPSSGGTYOCLK 180
 |||||||
 Db 218 GYIPSKFPNNLKKKNYCRNPDRPWCFTTDPKRWELCDIPRCTPPSSGGTYOCLK 277
 |||||||
 QY 181 GTGENYGNVAVTYSGHTCOHWSAQTPHTHERTPENPCKNLDENYCRNPDGKRAPWCHT 240
 |||||||
 Db 278 GTGENYGNVAVTYSGHTCOHWSAQTPHTHERTPENPCKNLDENYCRNPDGKRAPWCHT 337
 |||||||
 QY 241 TNSQVRWEYCKIPSCDSSPV 260
 |||||||
 Db 338 TNSQVRWEYCKIPSCDSSPV 357
 |||||||

RESULT 2

B30848
 Plasmin (EC 3.4.21.7) precursor - rhesus macaque
 C:Species: Macaca mulatta (rhesus macaque)
 C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
 C:Accession: B32869; B30848
 R:Tomlinson, J.E.; McLean, J.W.; Lawm, R.M.
 J. Biol. Chem. 264, 5957-5965, 1989
 A:Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
 A:Reference number: A32869; M0ID:89174660
 A:Accession: B32869
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1810 <TOM>
 A:Cross-references: GB:J04697; NID:9342272; PIDN:AAA36901.1; PID:9342273
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>
 F:1-9/Domain: signal sequence #status predicted <SIG>
 F:103-181/Domain: kringle homology <KR1>
 F:185-262/Domain: kringle homology <KR2>
 F:275-352/Domain: kringle homology <KR3>
 F:377-454/Domain: kringle homology <KR4>
 F:481-560/Domain: kringle homology <KR5>
 F:581-803/Domain: trypsin homology <TRY>
 F:49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
 bonds: #status predicted
 F:622,665,760/Active site: His, Asp, Ser #status predicted

Query Match 93.6%; Score 1442; DB 2: Length 810;
 Best Local Similarity 93.1%; Pred. No. 4.5e-98;
 Matches 242; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 VYLSECTGNGKNGKNGYRGMTSKNGITCOKWSSTPHRRPSPATHPSEGLEENYCRPNPN 60
 |||||||
 Db 98 VYLSECTGNGKNGKNGYRGMTSKNGITCOKWSSTPHRRPSPATHPSEGLEENYCRPNPN 157
 |||||||

QY 61 DPGSPWCYTTPDEPKRYDCILCEEECMHCSGENYDGKISKTNGLGECQAMDSQSPHAA 120
 |||||||
 Db 158 DPGSPWCYTTPDEPKRYDCILCEEECMHCSGENYDGKISKTNGLGECQAMDSQSPHAA 217
 |||||||
 QY 121 GYIPSKFPNNLKKKNYCRNPDRPWCFTTDPKRWELCDIPRCTPPSSGGTYOCLK 180
 |||||||
 Db 218 GYIPSKFPNNLKKKNYCRNPDRPWCFTTDPKRWELCDIPRCTPPSSGGTYOCLK 277
 |||||||
 QY 181 GTGENYGNVAVTYSGHTCOHWSAQTPHTHERTPENPCKNLDENYCRNPDGKRAPWCHT 240
 |||||||
 Db 278 GTGENYGNVAVTYSGHTCOHWSAQTPHTHERTPENPCKNLDENYCRNPDGKRAPWCHT 337
 |||||||
 QY 241 TNSQVRWEYCKIPSCDSSPV 260
 |||||||
 Db 338 TNSQVRWEYCKIPSCDSSPV 357
 |||||||

RESULT 3

PLPG
 plasmin (EC 3.4.21.7) precursor - pig (fragment)
 N:Alternate names: plasminogen
 N:Contains: miniplasminogen
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
 C:Accession: S03733; S03737; A25834
 R:Schaller, J.; Marti, T.; Roesselet, S.J.; Kaempfer, U.; Rickli, E.E.
 Fibrinolysis 1, 91-102, 1987
 A:Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the
 A:Reference number: S03733
 A:Accession: S03733
 A:Molecule type: protein
 A:Residues: 1-560 <SCH>
 R:Brundisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg,
 Eur. J. Biochem. 114, 465-470, 1981
 A:Title: Comparison of the primary structure of the N-terminal CNBr fragments of huma
 A:Reference number: S03735; M0ID:81212097
 A:Accession: S03737
 A:Molecule type: protein
 A:Residues: 1-57 <BRU>
 R:Marti, T.; Schaller, J.; Rickli, E.E.
 Eur. J. Biochem. 149, 279-285, 1985
 A:Title: Determination of the complete amino-acid sequence of porcine miniplasminogen
 A:Reference number: A25834; M0ID:85203907
 A:Accession: A25834
 A:Molecule type: protein
 A:Residues: 450-790 <MAR>
 C:Function:
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a
 us the walls of the graafian follicle; also activates the urokinase-type plasminogen
 A:Pathway: fibrinolysis
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine pr
 F:1-790/Product: plasminogen #status predicted <PRO>
 F:1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>
 F:1-77/Domain: activation peptide #status predicted <APY>
 F:78-560/Product: plasmin chain A #status predicted <ACH>
 F:84-162/Domain: kringle homology <KR1>
 F:166-243/Domain: kringle homology <KR2>
 F:256-333/Domain: kringle homology <KR3>
 F:358-435/Domain: kringle homology <KR4>
 F:450-790/Product: miniplasminogen #status experimental <MIN>
 F:461-540/Domain: kringle homology <KR5>
 F:561-790/Product: plasmin chain B #status experimental <BCH>
 F:30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,
 bonds: #status predicted
 F:602,645,740/Active site: His, Asp, Ser #status predicted

Query Match 83.9%; Score 1292; DB 1: Length 790;
 Best Local Similarity 81.4%; Pred. No. 4e-87;
 Matches 210; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

QY 1 VYISECKTGNGKNGRGTMTKNGITQCKWSSTSPHRRSPATHPSEGLEENYCRNPDN 60
 Db IYLLSECKTGNGKNGRGTMTKNGITQCKWSSTSPHRRSPATHPSEGLEENYCRNPDN 138
 QY 61 DPGPMCTTDPDKRYDCDILECEECMHCSCGENTGKISTKMTSGLECOAMDOSPHAH 120
 Db DEKGPWCYTTPDPRDYCDIPCECECMHCSCGENTGKISTKMTSGLECOAMDOSPHAH 198
 QY 121 GYIPSKFPNNKLNKKNYCRNDRELPRMCFPTTDPNKRMELCDIPRCTTPPSSGPTQCLK 180
 Db GYIPSKFPNNKLNKKNYCRNDRELPRMCFPTTDPNKRMELCDIPRCTTPPSSGPTQCLK 258
 QY 181 GTGENTRGNAVAVYSGHTCOHWSAQTPHTHERPPENPCKNLNDENYCRNDGKRAAPWCHT 240
 Db GTGENTRGNAVAVYSGHTCOHWSAQTPHTHERPPENPCKNLNDENYCRNDGKRAAPWCHT 318
 QY 241 TNSQVRMEYCKIPSCDSS 258
 Db TNSQVRMEYCKIPSCDSS 336
 QY 319 TQSEVRMDYCKIPSCDSS 336

RE 4
 PL 4
 plasmin (EC 3.4.21.7) precursor - bovine
 N:Alternate names: plasminogen
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Sep-1987 #sequence, revision 28-Apr-1995 #text_change 18-Jun-1999
 R:Accession: S45046; A25835; I45961; S03736
 R:Berghlund, L.; Andersen, M.D.; Petersen, T.E.
 submitted to the EMBL Data Library, May 1994
 A:Description: Cloning and characterization of the bovine plasminogen cDNA.
 A:Reference number: S45046
 A:Accession: S45046
 A:Molecule type: mRNA
 A:Residues: 1-812 <BER>
 A:Cross-references: EMBL:X79402; NID:g494962; PIDN:CAAS5939.1; PID:g494963
 A:Experimental source: Liver
 A:Note: It is uncertain whether Met-1 or Met-8 is the initiator
 R:Schallier, J.; Moser, P.W.; Danneberger-Muller, G.A.K.; Rosselet, S.J.; Kampfer, U.; Rick
 Eur. J. Biochem. 149, 267-278, 1985
 A:Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plasmin
 A:Reference number: A25835; MUID:85203906
 A:Accession: A25835
 A:Molecule type: protein
 A:Residues: 27-334, 'D', 336-515, 'H', 517-554, 'L', 556-812 <SCH>
 R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
 Biochemistry 23, 4243-4250, 1984
 A:Title: Characterization of a complementary deoxyribonucleic acid coding for human and
 A:Reference number: I45961; MUID:85023311
 A:Accession: I45961
 A:Note: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 706-743, 'R', 745-812 <MAL>
 A:Cross-references: GB:K02935; NID:g163551; PIDN:AAA30714.1; PID:g163552
 R:Brundish, R.A.; Lersch, P.G.; Schallier, J.; Rickli, E.E.; Lergler, W.; Manneberg, M.;
 Eur. J. Biochem. 114, 465-470, 1981
 A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of human,
 A:Reference number: S03735; MUID:81212097
 A:Accession: S03735
 A:Molecule type: protein
 A:Residues: 27-83 <BRU>
 C:Function:
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
 as the walls of the graafian follicle; also activates the urokinase-type plasminogen act
 A:Pathway: fibrinolysis
 C:Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology
 C:Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringe; plasma;
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:8-103/Domain: plasminogen-related protein precursor homology <PLPH>
 F:27-103/Product: plasminogen #status experimental <PRO>
 F:27-103/Domain: activation plasmin #status experimental <APT>
 F:104-583-812/Product: plasmin chain A #status experimental <ACH>
 F:104-583/Domain: plasmin chain A #status experimental <ACH>

F:110-188/Domain: kringe homology <KR1>
 F:152-269/Domain: kringe homology <KR2>
 F:282-359/Domain: kringe homology <KR3>
 F:384-461/Domain: kringe homology <KR4>
 F:485-564/Domain: kringe homology <KR5>
 F:584-812/Domain: plasmin chain B #status experimental <BCH>
 F:584-805/Domain: trypsin homology <TRY>
 F:56-80, 60-68, 110-188, 131-171, 159-183, 192-269, 195-323, 213-252, 241-264, 282-359, 303-342
 bonds: #status predicted
 F:315/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:365/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F:624, 667, 762/Active site: His, Asp, Ser #status predicted

Query Match 83.8%; Score 1291; DB 1; Length 812;
 Best Local Similarity 80.8%; Pred. No. 4, 9e-87;
 Matches 210; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 VYISECKTGNGKNGRGTMTKNGITQCKWSSTSPHRRSPATHPSEGLEENYCRNPDN 60
 Db IYLLSECKTGNGKNGRGTMTKNGITQCKWSSTSPHRRSPATHPSEGLEENYCRNPDN 164
 QY 61 DPGPMCTTDPDKRYDCDILECEECMHCSCGENTGKISTKMTSGLECOAMDOSPHAH 120
 Db DPGPMCTTDPDKRYDCDILECEECMHCSCGENTGKISTKMTSGLECOAMDOSPHAH 224
 QY 121 GYIPSKFPNNKLNKKNYCRNDRELPRMCFPTTDPNKRMELCDIPRCTTPPSSGPTQCLK 180
 Db GYIPSKFPNNKLNKKNYCRNDRELPRMCFPTTDPNKRMELCDIPRCTTPPSSGPTQCLK 284
 QY 181 GTGENTRGNAVAVYSGHTCOHWSAQTPHTHERPPENPCKNLNDENYCRNDGKRAAPWCHT 240
 Db GTGENTRGNAVAVYSGHTCOHWSAQTPHTHERPPENPCKNLNDENYCRNDGKRAAPWCHT 344
 QY 241 TNSQVRMEYCKIPSCDSSPV 260
 Db TNSQVRMEYCKIPSCDSSPV 364

RESULT 5
 PLMS
 plasmin (EC 3.4.21.7) precursor - mouse
 N:Contains: angiotatin; plasminogen
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Sep-1991 #sequence, revision 01-Nov-1996 #text_change 18-Jun-1999
 R:Accession: A38514; S48202; S48203
 R:Deegen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
 Genomics 8, 45-61, 1990
 A:Title: Characterization of the cDNA coding for mouse plasminogen and localization o
 A:Reference number: A38514; MUID:91184812
 A:Accession: A38514
 A:Molecule type: mRNA
 A:Residues: 1-812 <DEG>
 A:Cross-references: GB:J04766; NID:g200402; PIDN:AAA50168.1; PID:g200403
 R:Lijnen, H.R.; Van Hoef, B.; Beelen, V.; Collen, D.
 Eur. J. Biochem. 224, 863-871, 1994
 A:Title: Characterization of the murine plasma fibrinolytic system.
 A:Reference number: S48202; MUID:95010076
 A:Accession: S48202
 A:Molecule type: protein
 A:Residues: 20-25 <LIJ>
 A:Accession: S48203
 A:Molecule type: protein
 A:Residues: 22-27 <LIJ>
 C:Comment: Plasminogen is synthesized by the kidney and is present in plasma and many
 immediately after dissociation from the clot. In the presence of the inhibitor, the act
 e inhibitor, the activation involves also removal of the activation peptide.
 C:Comment: Stromelysin 1 (see PIR:KCMS1) acts on plasminogen to produce angiotatin.
 C:Function:
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a
 ns the walls of the graafian follicle; also activates the urokinase-type plasminogen

RESULT 8
JH0579
hepatocyte growth factor precursor [validated] - human
N:Alternate names: hepatopietin A; scatter factor
C:Species: Homo sapiens (man)
C:Date: 17-Aug-1992 #sequence; revision 17-Aug-1992 #text; change 08-Dec-2000
C:Accession: JH0579; J00333; A41140; B36677; A33512; A39006; PH0114; A37796; S06
R:Seiki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.
Gene 102, 213-219, 1991
A:Title: Organization of the human hepatocyte growth factor-encoding gene.
A:Reference number: JH0579; MUID:91340155
A:Accession: JH0579
A:Molecule type: DNA
A:Residues: 1-728 <SEK>
A:Cross-references: DBJ:D90318
A:Note: The authors translated the codon GAA for residue 662 as Gly
R:Seiki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.
Submitted to JFID, March 1991
A:Description: Organization of the human hepatocyte growth factor-encoding gene.
A:Reference number: J00333
A:Accession: J00333
A:Molecule type: DNA
A:Residues: 1-481, 'RT', 484-728 <SE2>
R:Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, H.
Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
A:Title: Evidence for the identity of human scatter factor and human hepatocyte growth f
A:Reference number: A41140; MUID:91334393
A:Accession: A41140
A:Molecule type: mRNA
A:Residues: 1-728 <WE1>
A:Cross-references: GB:WJ3239; NID:9337935; PIDN:AA64239.1; PID:9337936
R:Seiki, T.; Ihara, I.; Sugimura, A.; Shimomishi, M.; Nishizawa, T.; Asami, O.; Hagiya, M.
Biochem. Biophys. Res. Commun. 172, 321-327, 1990
A:Title: Isolation and expression of cDNA for different forms of hepatocyte growth fact
A:Reference number: A36677; MUID:91025062
A:Accession: B36677
A:Molecule type: mRNA
A:Residues: 1-728 <SE3>
A:Cross-references: GB:M60718; NID:9184031; PIDN:AA52648.1; PID:9184032
A:Accession: A36677
A:Molecule type: mRNA
A:Residues: 1-161, 167-728 <SE4>
A:Cross-references: EMBL:X16323
A:Experimental source: leukocyte
R:Miyaizawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya
Biochem. Biophys. Res. Commun. 163, 967-973, 1989
A:Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth fac
A:Reference number: A33512; MUID:89392017
A:Accession: A33512
A:Note: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-728 <M1Y>
A:Cross-references: GB:M29145; NID:9184041; PIDN:AA52650.1; PID:9306846
R:Rubin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Hitt
Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991
A:Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocy
A:Reference number: A39006; MUID:91110540
A:Accession: A39006
A:Molecule type: mRNA
A:Residues: 1-161, 167-728 <RUB>
A:Cross-references: GB:M55379
A:Experimental source: embryonic lung
R:Yoshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.; Nakayama,
Biochem. Biophys. Res. Commun. 175, 660-667, 1991
A:Title: Identification of the N-terminal residue of the heavy chain of both native and
A:Reference number: PH0114; MUID:91207365
A:Accession: PH0114
A:Molecule type: protein
A:Residues: 32-43; 53-58 <YOS>
R:Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.
J. Cell Biol. 111, 2097-2108, 1990

A:Title: Scatter factor: molecular characteristics and effect on the invasiveness of
A:Reference number: A37796; MUID:91035621
A:Accession: A37796
A:Molecule type: protein
A:Residues: 86-91; 329-344; 356-363, 'XX', 366-370; 425-434; 442-447, 'X', 449-450; 543-546, 'X
R:Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seiki, T.; Shimomishi, M.; Sugimura, A.; Ta
Nature 342, 440-443, 1989
A:Title: Molecular cloning and expression of human hepatocyte growth factor.
A:Reference number: S06794; MUID:90066676
A:Accession: S06794
A:Molecule type: mRNA
A:Residues: 1-31, 'HK', 34-77, 'N', 79-292, 'V', 294-299, 'W', 301-316, 'A', 318-335, 'K', 337-38
A:Cross-references: EMBL:X16323; NID:932081; PIDN:CAA34587.1; PID:932082
A:Experimental source: liver
A:Note: the authors translated the codon CAG for residue 727 as Glu
R:Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Bir
Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
A:Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth f
A:Reference number: I59214; MUID:93087571
A:Accession: I59214
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-288, 'ET', <HAR>
A:Cross-references: GB:I02931; NID:9184033; PIDN:AA52649.1; PID:9184034
R:Miyaizawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.
Eur. J. Biochem. 197, 15-22, 1991
A:Title: An alternatively processed mRNA generated from human hepatocyte growth facto
A:Reference number: S15443; MUID:91200041
A:Accession: S15443
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-288, 'ET', <M1Y2>
A:Cross-references: EMBL:X57574; NID:932083; PIDN:CAA40802.1; PID:932084
R:Shim, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.
Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991
A:Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibroblasts: clon
A:Reference number: I52253; MUID:92062058
A:Accession: I52253
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 161-166 <SHI>
A:Cross-references: GB:S62561; NID:9237996; PIDN:AA620169.1; PID:9237997
C:Genetics:
A:Gene: GDB:HGF
A:Cross-references: GDB:127524; OMIM:142409
A:Map position: 7q21.1-7q21.1
A:Introns: 30/71, 85/72, 123/71, 161/72, 209/71, 249/72, 289/71, 347/72, 390/71, 424/72, 469/71,
C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C:Function:
A:Description: stimulates mitosis of hepatocytes and other cells
A:Note: does not have proteinase activity
C:Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle;
F:1-31/Domain: signal sequence #status predicted <SIC>
F:32-494/Domain: alpha chain #status experimental <ACH>
F:128-206/Domain: kringle homology <KR1>
F:211-288/Domain: kringle homology <KR2>
F:305-383/Domain: kringle homology <KR3>
F:391-469/Domain: kringle homology <KR4>
F:495-728/Domain: beta chain #status experimental <BCH>
F:495-716/Domain: trypsin homology <TRY>
F:32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status expert
F:294,402,566,655/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:487-604/Disulfide bonds: #status predicted

Query Match 51.8%; Score 797; DB 1; Length 728;
Best Local Similarity 51.0%; Pred. No. 5; Se-51;
Matches 134; Conservative 42; Mismatches 81; Indels 6; Gaps 4;
OY 2 YLSECKTGNGKNYRGTMSTKNGICGCKWSSTSPHRRPSPATPSEGLEENYCRPNPD 61

OY 240 TTNSGVWRYXC-KIPSCDS 258
11 : : : : :
Db 351 TTDPNIRIGHCSQIKKCOAS 370

RESULT 11
A60185
hepatocyte growth factor precursor - mouse
N:Alternate names: hepatoleitin A; scatter factor
C:Species: Mus musculus (house mouse)
C>Date: 03-Mar-1993 #sequence_revision 26-May-1994 #text_change 16-Jun-2000
C:Accession: J02117; PC2064; A60185; S43416; S45521; S17173; S10966; I48758; J00231
R:Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.
R:Biochem. Biophys. Res. Commun. 199, 772-779, 1994
A>Title: Identification of mouse mammary fibroblast-derived mammary growth factor as hep
A:Reference number: J02117; MWID:94183257
A:Accession: J02117

A:Molecule type: mRNA
A:Residues: 1-728 <SAS>
A:Cross-references: GB:D10212; NID:g220435; PIDN:BA01064.1; PID:g220436
A:Experimental source: Fibroblast, COS-1 cell
A:Submitted to JRPD, May 1993
A:Accession: PC2064

A:Molecule type: protein
A:Residues: 496-507 <S&Z>
R:Rosen, E.M.; Meromsky, L.; Setter, E.; Winter, D.W.; Goldberg, I.D.
Proc. Soc. Exp. Biol. Med. 195, 34-43, 1990
A>Title: Purified scatter factor stimulates epithelial and vascular endothelial cell mig
A:Reference number: A60185; MWID:90377927
A:Accession: A60185

A:Molecule type: protein
A:Residues: 'X', 184-188, 'KX', 191-192, 'X', 194, 'XX', 197, 357-364, 'XX', 367, 375-377, 'E', 379,
R:Liu, Y.; Michalopoulos, G.K.; Zarnegar, R.
Biochim. Biophys. Acta 1216, 299-303, 1993
A>Title: Molecular cloning and characterization of cDNA encoding mouse hepatocyte growth
A:Reference number: S43416; MWID:94060105
A:Accession: S43416

A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-728 <LIU>
A:Cross-references: EMBL:X72307
R:Liu, Y.
submitted to the EMBL Data Library, May 1993
A:Reference number: S45521
A:Accession: S45521

A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-563, 'H', 565-728 <LI2>
A:Cross-references: EMBL:X72307
R:Berger, A.; Fellous, J.; Young, S.; Pappin, D.; Rahman, D.
Biochem. J. 278, 35-41, 1991
A>Title: Purification and characterization of biologically active scatter factor from ra
A:Reference number: S17173; MWID:91354223
A:Accession: S17173

A:Molecule type: protein
A:Residues: 496-517, 'T', 519 <COF>
R:Gherardi, E.; Stoker, M.
Nature 346, 228, 1990
A>Title: Hepatocytes and scatter factor.
A:Reference number: S10966; MWID:90326152
A:Accession: S10966

A>Status: preliminary
A:Molecule type: protein
A:Residues: 496-507, 'X', 509-512, 'L', 514-516, 'X', 518-519 <NAT>
R:Piaschke-Schlutter, A.; Behrens, J.; Gherardi, E.; Birchmeier, W.
J. Biol. Chem. 270, 830-836, 1995
A>Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter.
A:Reference number: I48758; MWID:95122532
A:Accession: I48758

A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-30 <RES>
A:Cross-references: EMBL:X81630; NID:g673451; PIDN:CA057286.1; PID:g673452

C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C:Function:
A:Description: stimulates mitosis of hepatocytes and other cells
A:Note: does not have proteinase activity
C:Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle;
E:1-32/Domain: signal sequence #status predicted <SIG>
E:56-495,496-788/Product: hepatocyte growth factor #status predicted <MNT>
E:56-495/Domain: hepatocyte growth factor alpha chain #status predicted <MCH>
F:129-207/Domain: kringle homology <KR1>
F:212-289/Domain: kringle homology <KR2>
F:306-384/Domain: kringle homology <KR3>
F:392-470/Domain: kringle homology <KR4>
E:496-728/Domain: hepatocyte growth factor beta chain #status predicted <BGH>
E:496-719/Domain: trypsin homology <TRY>
E:332/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
E:293,403,509,656/Binding site: carboxylate (Asn) (covalent) #status predicted
:488-607/Disulfide Bonds: #status predicted

Query Match	50.4%;	Score 776;	DB 1;	Length 728;
Best Local Similarity	49.4%;	Pred. No. 1.9e-49;		
Matches 131;	Conservative	40;	Mismatches	84;
			Indels	10;
			Gaps	4.

[illegible]

RESULT 12

JC5061

macrophage-stimulating protein 1 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Jan-1997 #sequence Revision 16-Jun-2000

C:Accession: JC5061

R:Ohshiro, K.; Iwama, A.; Matsuno, K.; Ezaki, T.; Sakamoto, O.; Hamaguchi, I.; Takasu

Biochem. Biophys. Res. Commun. 227, 273-280, 1996

A:Title: Molecular cloning of rat macrophage-stimulating protein and its involvement

A:Reference number: JC5061; MUID:97011126

A:Accession: JC5061

A:Molecule type: mRNA

A:Residues: 1-716 <OHS>

A:Cross-references: EMBL:X95096; NID:g1669718; PIDD:CAN64473.1; PID:g1669719

C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor

C:Superfamily: hepatocyte growth factor; kringle homology; trypsin homology

C:Keywords: duplication; glycoprotein; growth factor; kringle

F:1-31/Domain: signal sequence #status predicted <SIG>

F:32-488,489-716/Product: macrophage-stimulating protein 1 #status predicted <MAT>

F:32-488/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <ACH>

F:110-186/Domain: kringle homology <KR11>

F:191-268/Domain: kringle homology <KR12>

F:292-370/Domain: kringle homology <KR13>

F:379-457/Domain: kringle homology <KR14>

F:468-716/Domain: macrophage-stimulating protein 1 beta chain #status predicted <BCH>

F:468-709/Domain: trypsin homology <TRY>

F:72,305,620/Binding site: carboxyrate (Asn) (covalent) #status predicted

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